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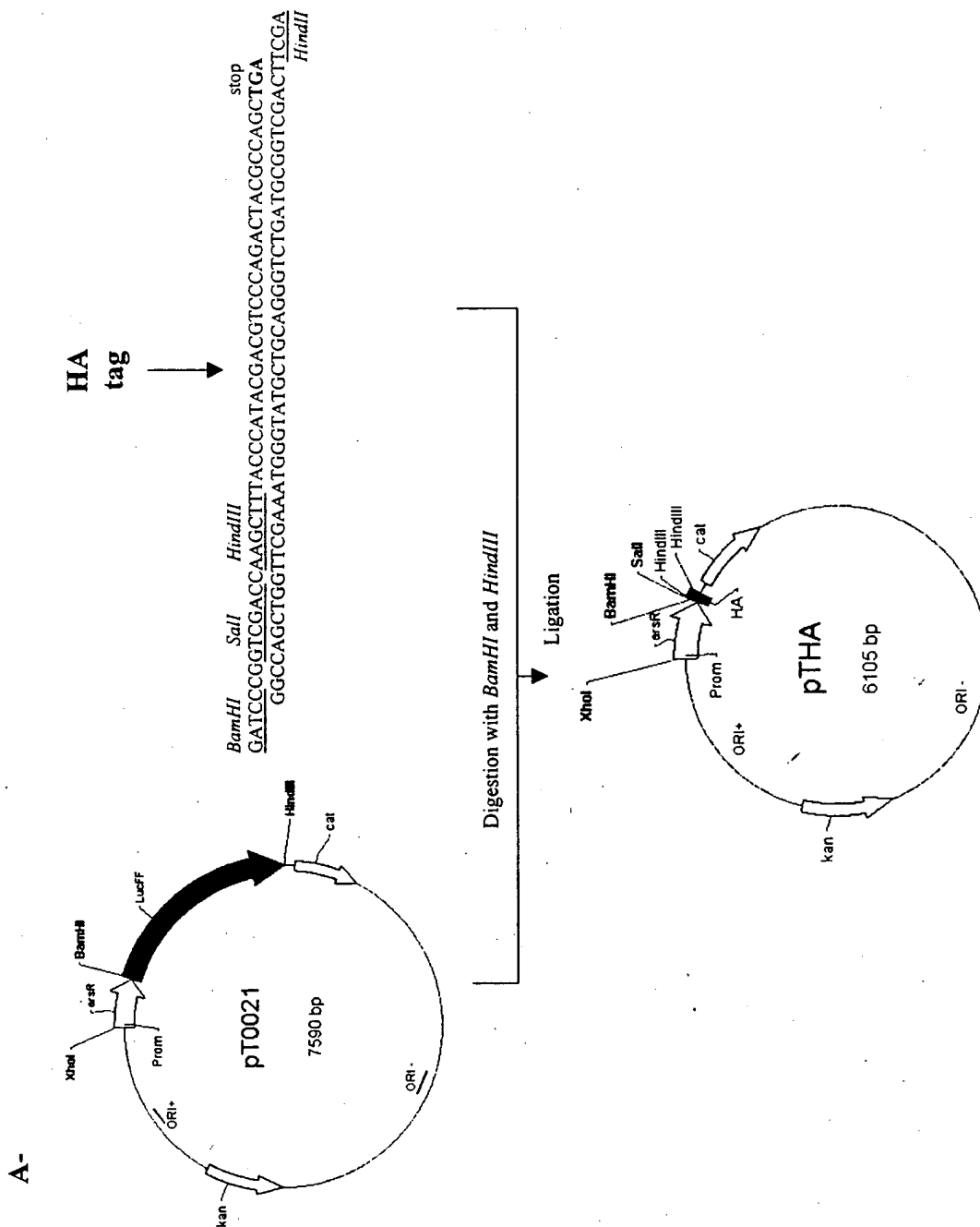
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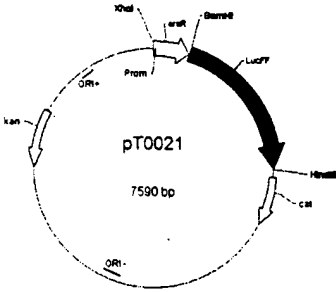
FIGURE 1A



B-

FIGURE 1B

PCR of pT0021 with XhoF and BamHNR



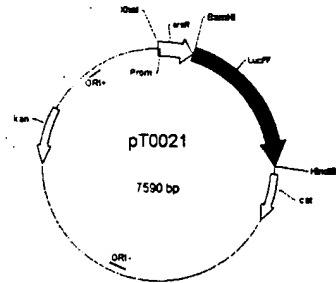
XhoF-5'-AATTCTCGAGTAAAAATACAT-3
XhoI

AAATCAGGTGACTGTTGAGAAAAGGAGGCGGATCCCG-BamHNR
Stop of
arsR RBS BamHI

Digestion with XhoI and BamHI

Ligation

PCR of pT0021 with LucFFB and LucFFH



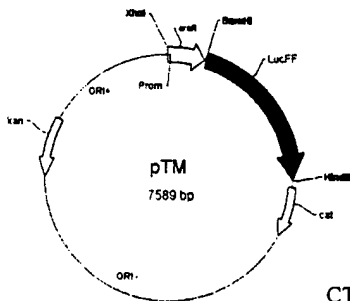
LucFFB-5'-CGGGATCCATGAGGGGTTCGAAGACG
BamHI Start Original BamHI
of LucFF was modified

GAAAGTCCAAATTGTAAGCTTGGG-LucFFH
Stop of HindIII
LucFF

Modified between stop
of arsR to BamHI

Digestion with BamHI and HindIII

Ligation



- Modified in the vicinity of BamHI
- Cloning site for ORFs: BamHI and HindIII
- No additional codons in the induced protein

Prom arsR LucFF
CTCGAG-----ATG-----TGAGAAAAGGAGGCGGATCCATG-----TAAGCTT
XhoI RBS BamHI HindIII

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FIGURE 1C

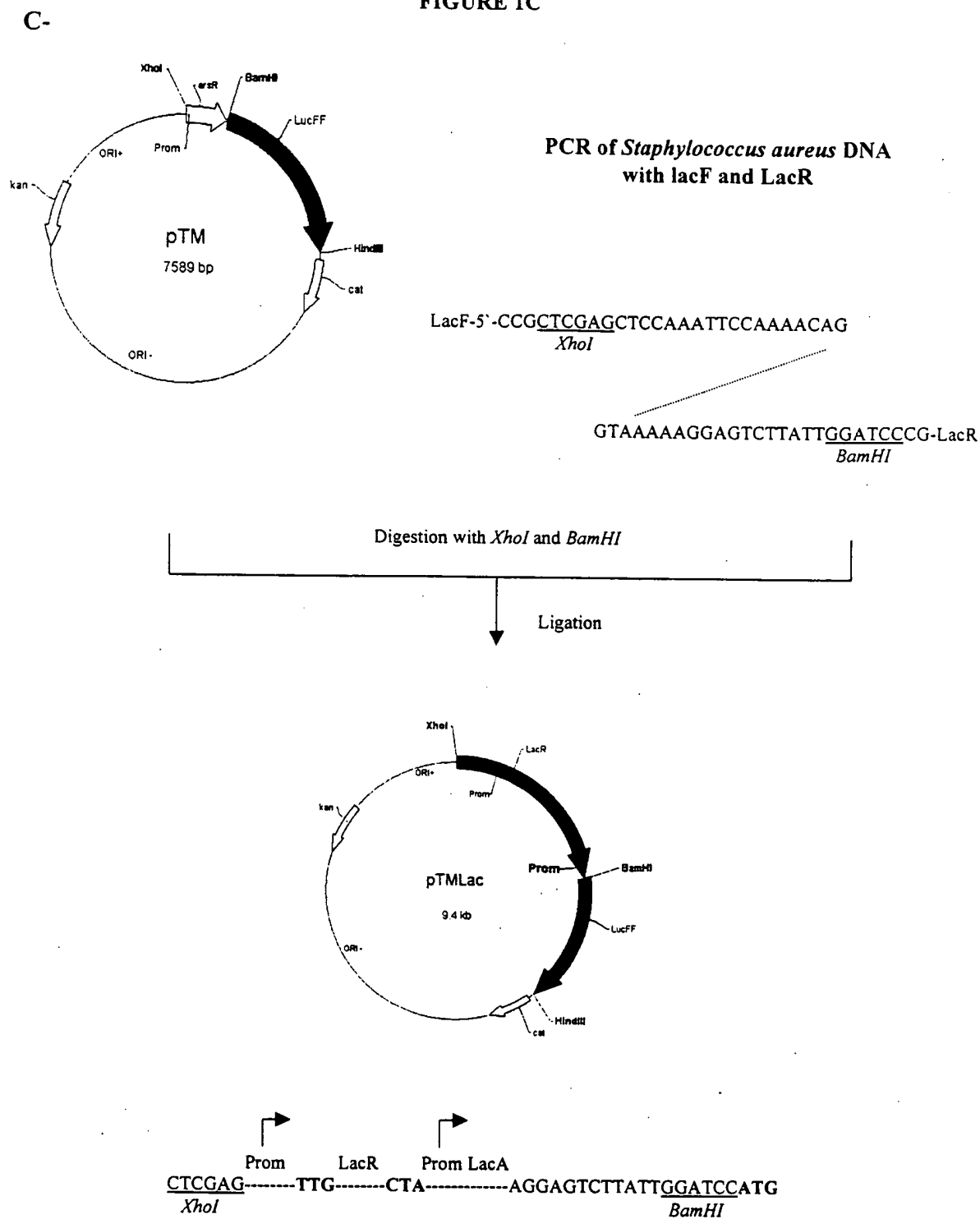
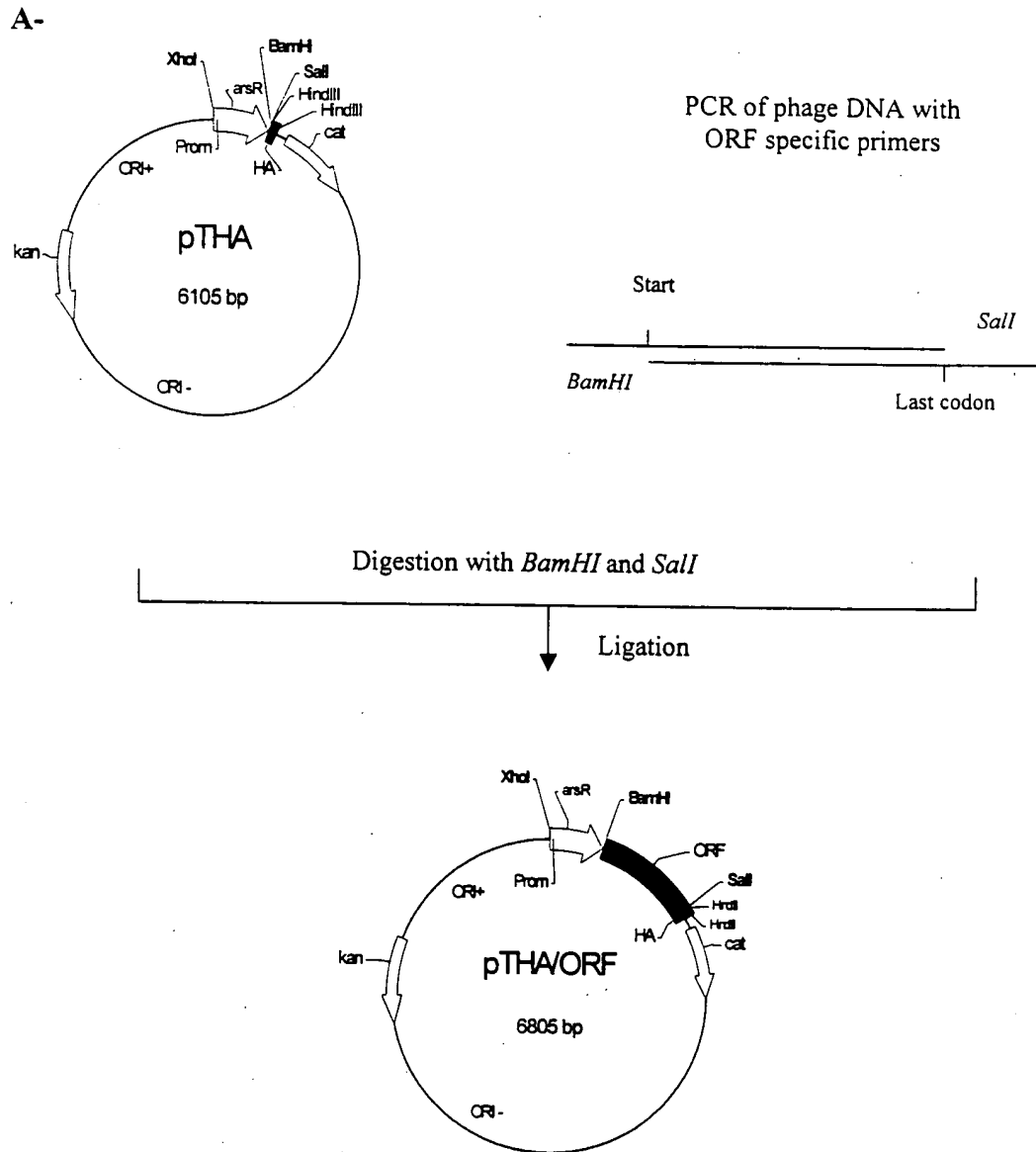


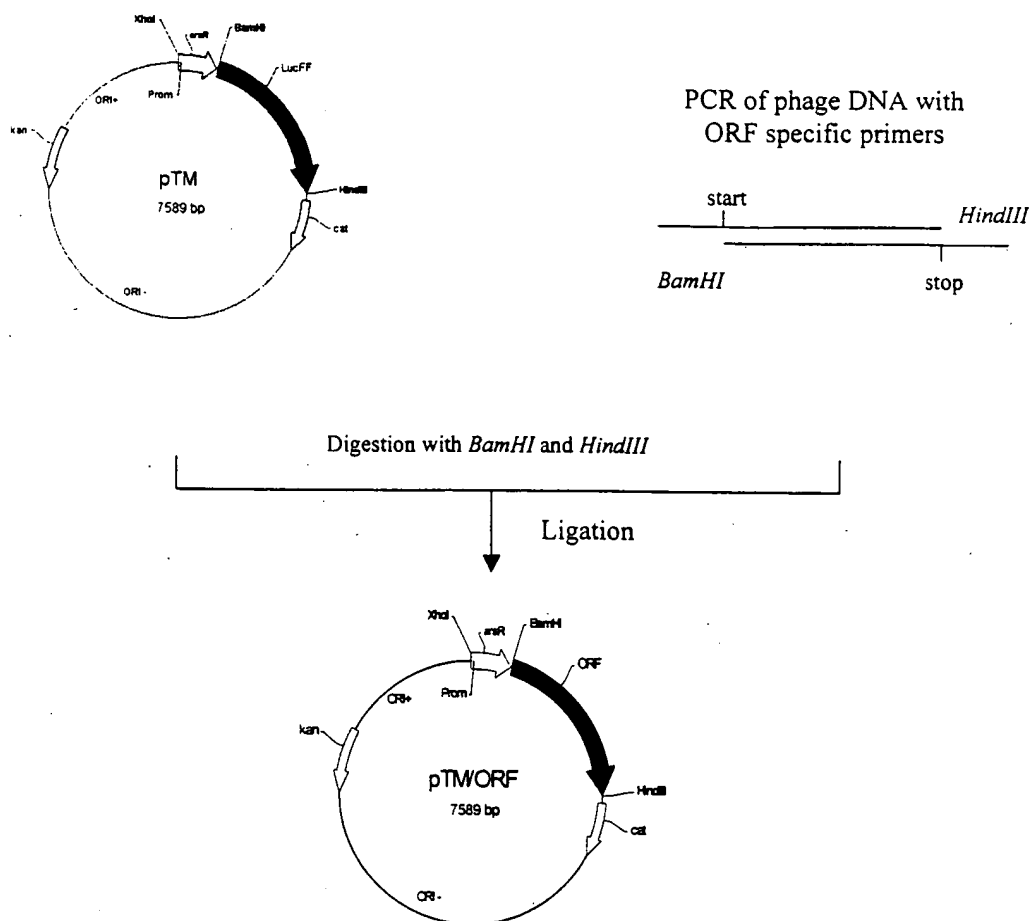
FIGURE 2A



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FIGURE 2B

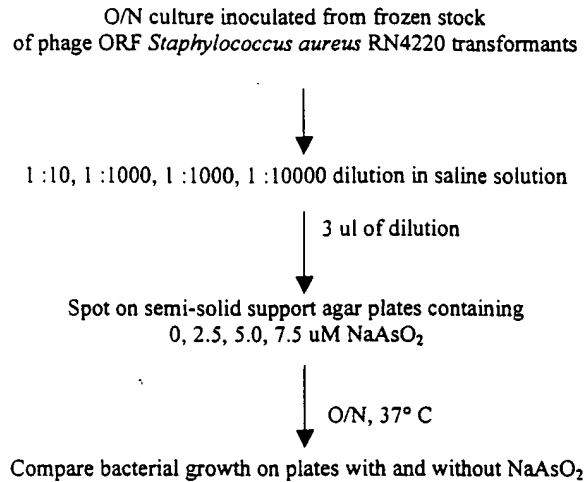
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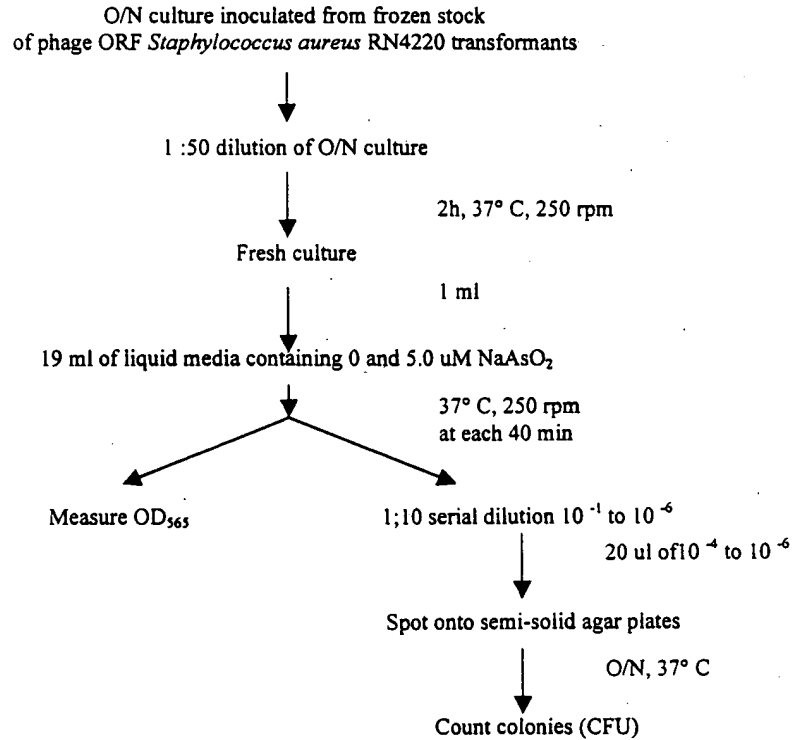
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FIGURE 3

A) Functional assay on semi-solid support medium



B) Functional assay in liquid medium



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FIGURE 4A

A-

44AHJD ORFs tested for functional analysis

UID	POS
44AHJDORF001	12627..10342
44AHJDORF002	3789..5732
44AHJDORF003	6626..8389
44AHJDORF004	8764..10227
44AHJDORF005	13890..12643
44AHJDORF006	803..2029
44AHJDORF007	2044..3027
44AHJDORF008	3020..3775
44AHJDORF009	5744..6496
44AHJDORF010	14420..13938
44AHJDORF011	15593..15225
44AHJDORF012	8391..8813
44AHJDORF013	14996..14586
44AHJDORF019	9836..9630
44AHJDORF023	6494..6315
44AHJDORF025	15175..14999
44AHJDORF027	12916..13080
44AHJDORF028	9235..9071
44AHJDORF035	13957..13811
44AHJDORF036	10165..10019
44AHJDORF039	1743..1883
44AHJDORF040	9740..9877
44AHJDORF044	12917..12783
44AHJDORF046	4891..5019
44AHJDORF048	15340..15212
44AHJDORF049	5784..5909
44AHJDORF053	3348..3467
44AHJDORF113	199..600
44AHJDORF114	16172..15870
44AHJDORF121	16362..16165
44AHJDORF123	614..796

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FIGURE 4B

B-








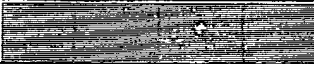
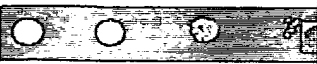





ORF ID	<i>Staphylococcus aureus</i> transformants	Semi-solid support media	
		Without induction	With induction (5 μ M sodium arsenite)
44AHJDORF12	Clone1		
	Clone2		
	Clone3		
44AHJDORF25	Clone1		
	Clone2		
	Clone3		
Control 77ORF30	Clone1		

FIGURE 5A

A-

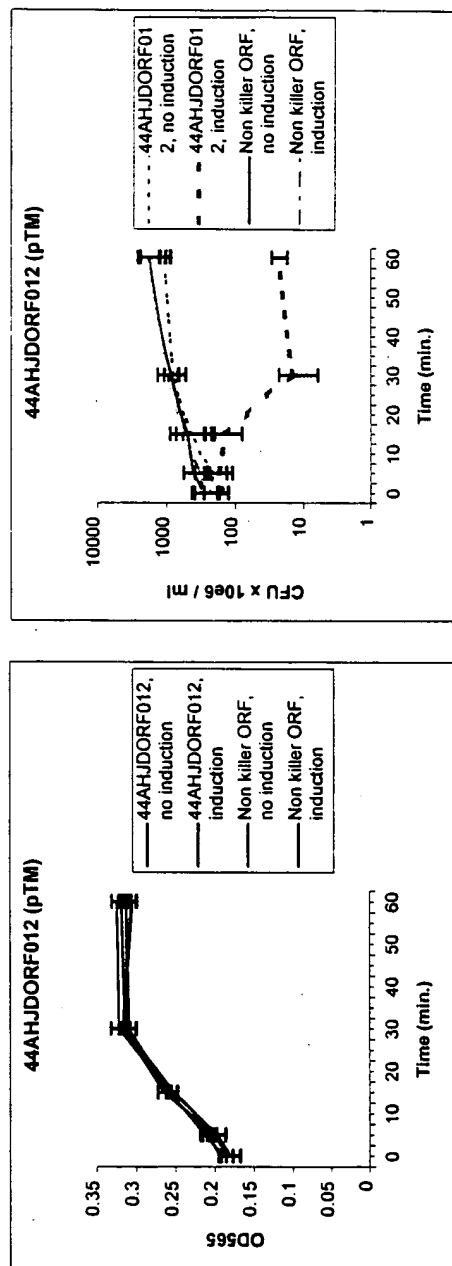
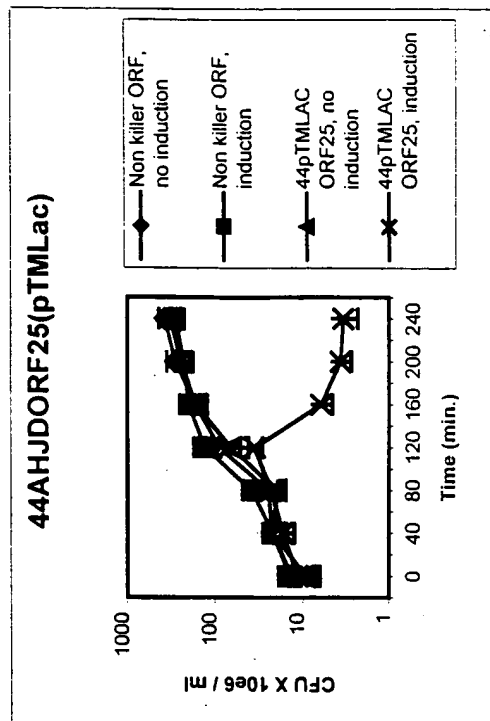
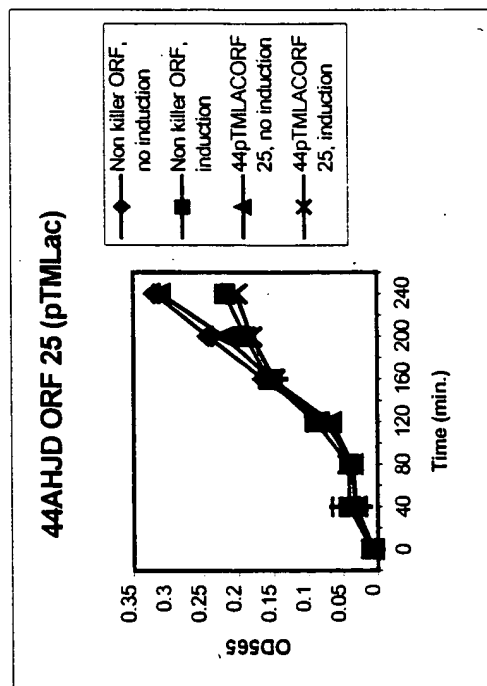
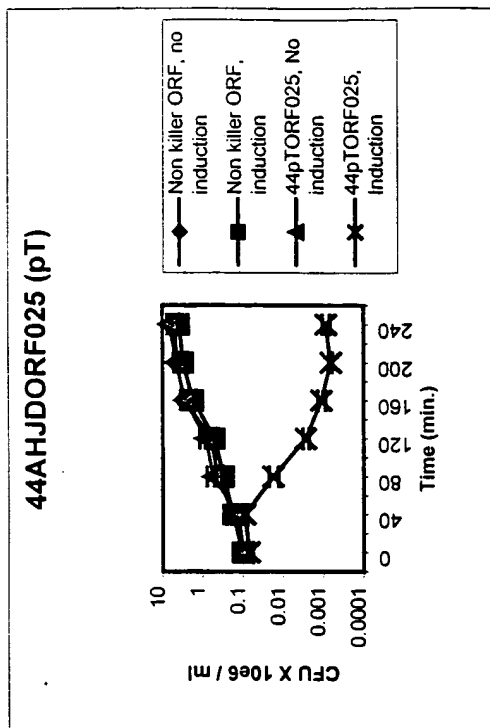
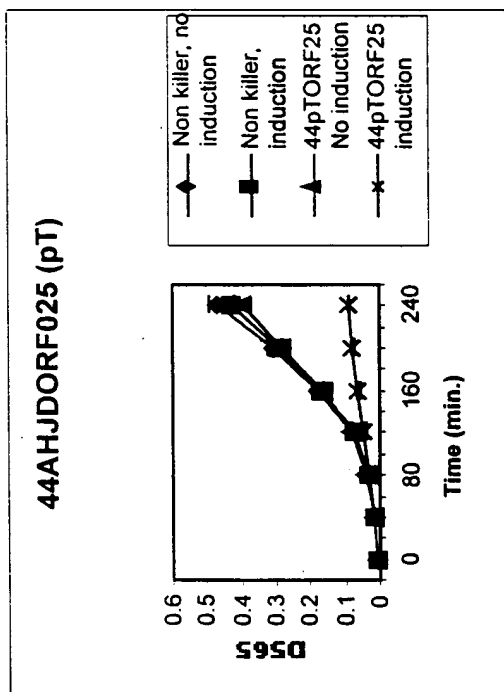


Fig
.5B



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FIGURE 6

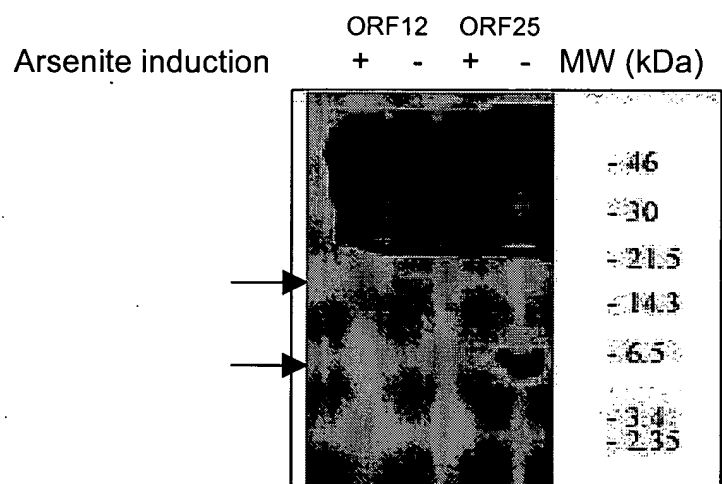
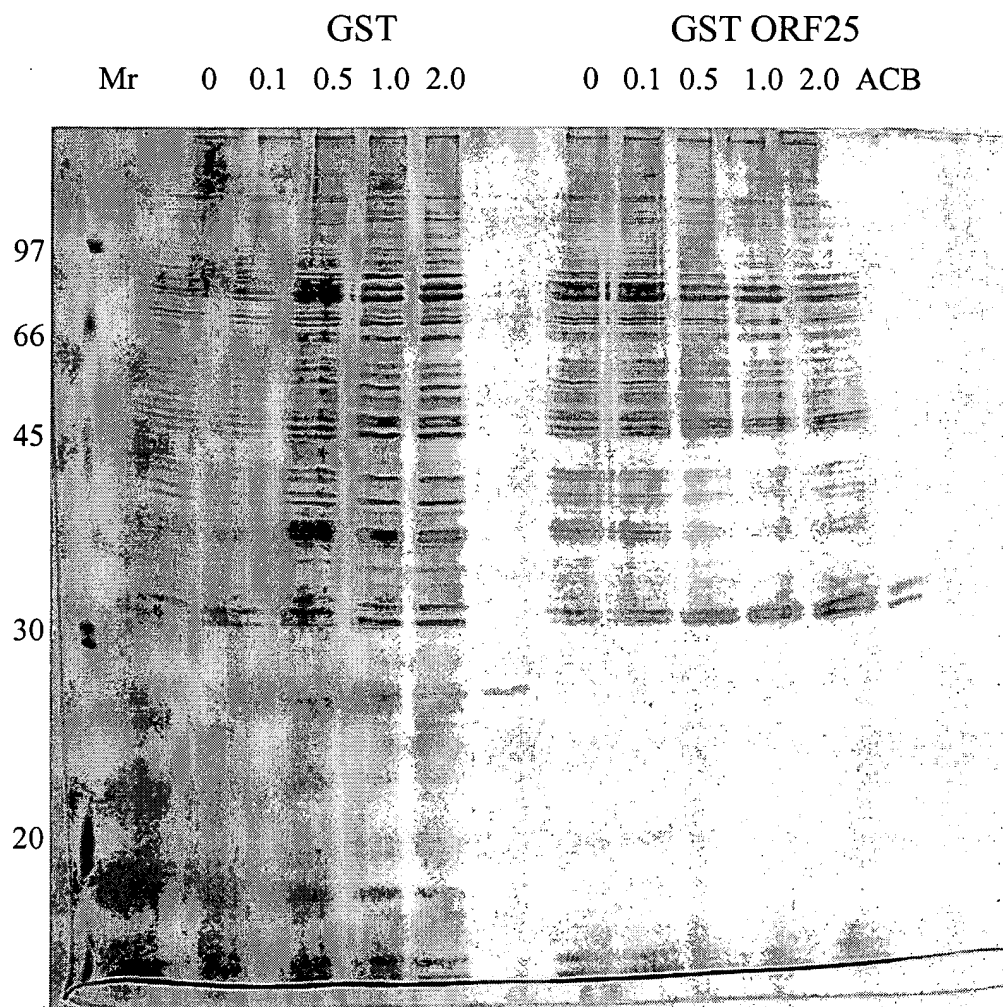
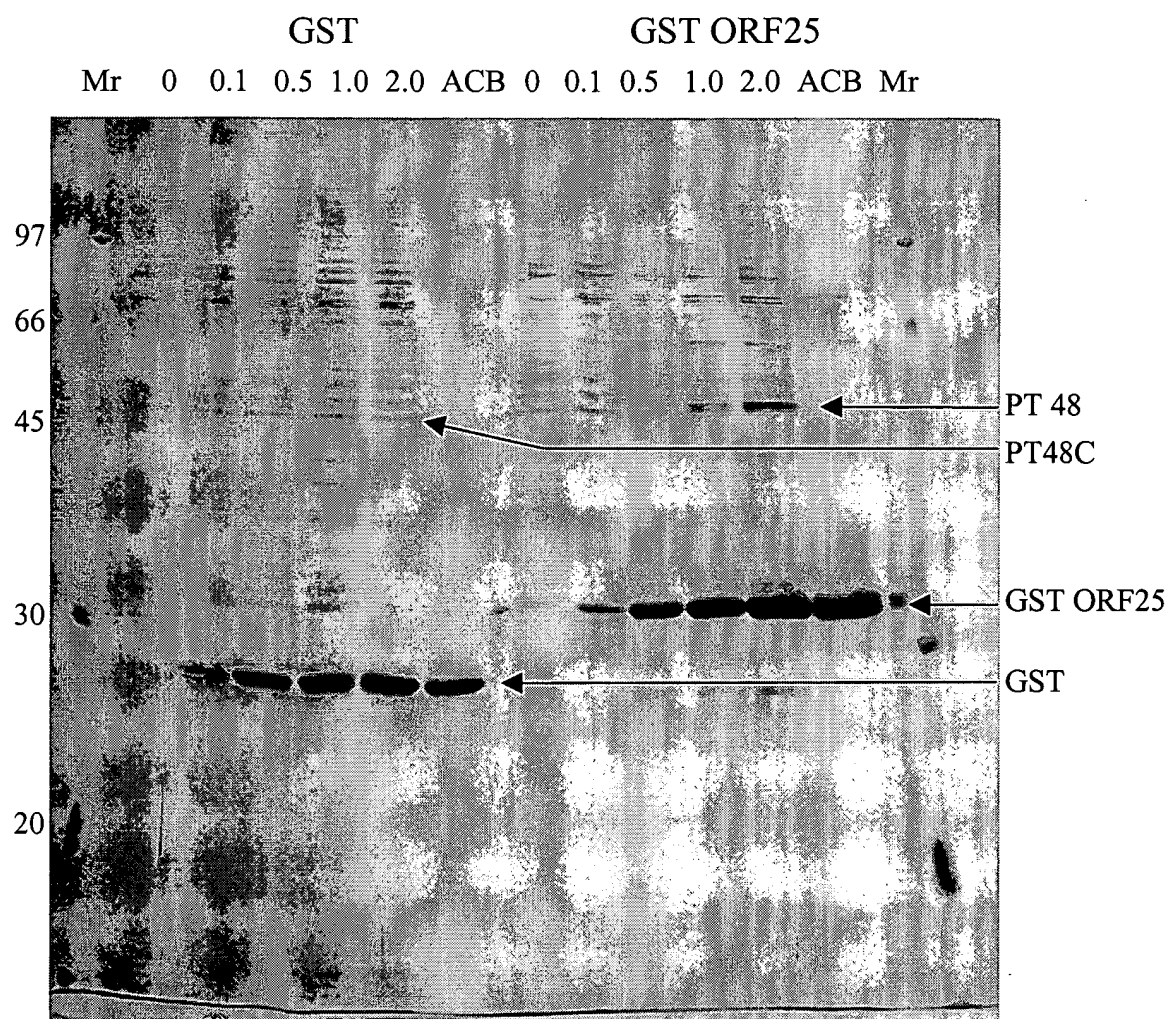


FIGURE 7A



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FIGURE 7B



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FIGURE 8

Tryptic peptide mass spectrum of 48 kDa interacting protein

(from Figure 1B)

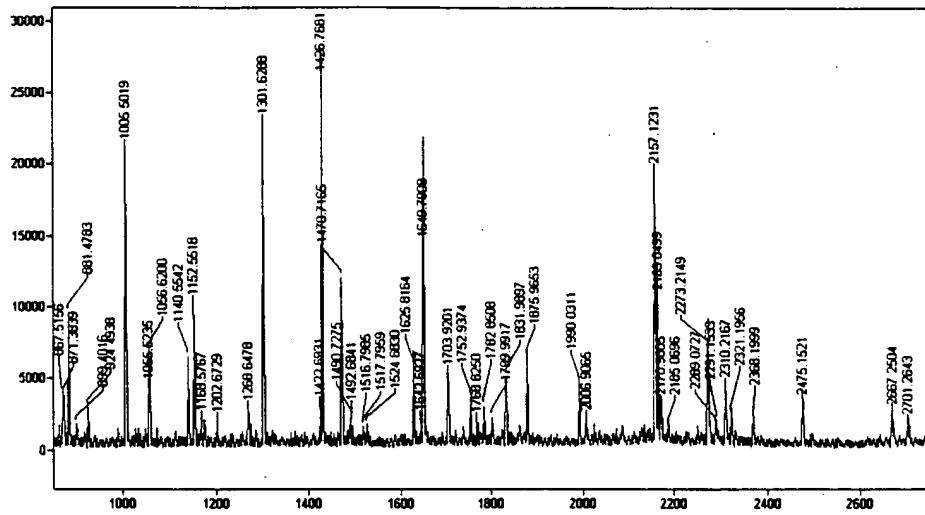
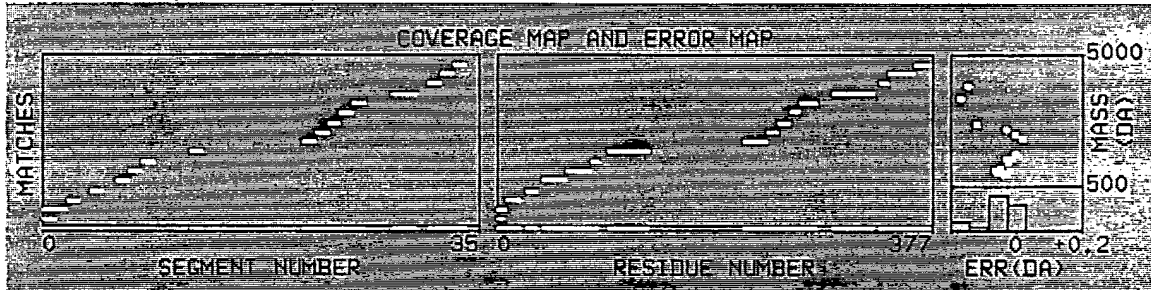


FIGURE 9

Identification of PT48 as DNA-directed DNA polymerase III beta.

Details for: PT48
gi|1706496|sp|P50029|DP3B-STAAU DNA POLYMERASE III, BETA CHAIN
gi|1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Staphylococcus aureus

Sample ID : PT 48
Number of Measured Peptides : 40
Number of Matched Peptides : 17
Coverage of protein sequence : 68%



Measured Mass(M)	Avg/ Mono	Computed Mass	Error (Da)	Residues Start	To	Missed Cut	Peptide sequence
870.370	M	870.397	-0.027	333	339	0	YMDALK
880.474	M	880.505	-0.032	82	88	0	FFVDIIK
898.392	M	898.429	-0.037	1	7	0	MMEFTIK
1004.492	M	1004.540	-0.048	235	243	0	VGNVNFISR
1054.514	M	1054.530	-0.016	1	8	1	MMEFTIKR
1055.603	M	1055.658	-0.055	26	35	0	TTLPTLTGK
1151.546	M	1151.586	-0.040	255	263	0	LEPENYEIK
1300.619	M	1300.641	-0.021	244	254	0	LEEGHYFDTR
1425.769	M	1425.782	-0.013	363	375	0	GDDSVTQLLPIR
1469.713	M	1469.740	-0.026	9	20	0	DYFITQLNDELK
1648.781	M	1648.784	-0.003	264	277	0	LSIDNGEFYHAIR
2156.112	M	2156.095	0.017	61	81	0	TVDGEDIVNISETGSVVLPGR
2309.198	M	2309.199	-0.000	40	60	0	EHEVLTGSDSEISIEITIPK
2474.139	M	2474.166	-0.027	214	234	0	IMSDNEEDIDIEFASNOVLFK
2666.266	M	2666.365	-0.099	340	362	0	AIDNDEVEVEFFGTMKPFILKPK
3577.670	A	3577.809	-0.139	292	326	1	LSTGDDVVELSSTSPETGTVKEEVDANDVEGGS�K
4033.298	A	4033.421	-0.123	97	132	0	LSTNEQFOTLITSGHSEFNLSGLDPDQYPLLPOVSR

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FIGURE 10

SEQ ID NO : 1 *Staphylococcus aureus* DnaN nucleotide sequence

ATGATGGAATTCACTATTAAGAGATTATTTTATTACACAATTAAATGACACATTA
GCTATTTACCAAGAACAACATTACCTATATTAAGTGGTATCAAAATCGATGCGAAAGAA
CATGAAGTTATATTAAGTGGTTCAGACTCTGAAATTTCAATAGAAATCACTATTCCTAAA
ACTGTAGATGGCGAAGATATTGTCAATATTTAGAAACAGGCTCAGTAGTACTTCCTGGA
CGATTCTTTGTTGATATTATAAAAAAATTACCTGGTAAAGATGTTAAATTATCTACAAAT
GAACAATTCAGACATTAATTACATCAGGTCAATCTGAATTTAATTTAAGTGGCTTAGAT
CCAGATCAATATCCTTTATTACCTCAAGTTTCTAGAGATGACGCAATTCAATTGTCGGTA
AAAGTGCTTAAAAACGTGATTGCACAAACAAATTTTGCAGTGTCCACCTCAGAAACACGC
CCAGTACTAACTGGTGTGAAGTGGCTTATACAAGAAAATGAATTAATATGCACAGCGACT
GACTCACACCGCTTGGCTGTAAGAAAGTTGCAGTTAGAAGATGTTTCTGAAAACAAAAAT
GTCATCATTCCAGGTAAGGCTTTAGCTGAATTAATAAAATTAATGTCGACAATGAAGAA
GACATTGATATCTTCTTTGCTTCAACCAAGTTTTATTTAAAGTTGGAAATGTGAACCTT
ATTTCTCGATTATTAGAAGGACATTATCCTGATACAACACGTTTATTCCTGAAAACCTAT
GAAATTAATAAGTATAGACAATGGGGAGTTTTATCATGCGATTGATCGTGCCTCTTTA
TTAGCGCGTGAAGGTGGTAATAACGTTATTAATAAGTACAGGTGATGACGTTGTTGAA
TTGTCTTCTACATCACCAGAAATTTGTTACTGTAAAAGAAGAAGTTGATGCAAACGATGTT
GAAGGTGGTAGCCTGAAAATTTCAATCAACTCTAAATATATGATGGATGCTTTAAAGCA
ATCGATAATGATGAGGTTGAAGTTGAATTCCTCGGTACAATGAAACCATTTATTCTAAAA
CCAAAAGGTGACGACTCGGTAACGCAATTAATTTTACCAATCAGAACTTACTAA

SEQ ID NO : 2 *Staphylococcus aureus* DnaN amino acid sequence

>gi|1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain -
Staphylococcus aureus

MMEFTIKRDYFITQLNDTLKAISPRITLPILTGKIDAKEHEVILTGSDSEISIEITIPKTVGDGDIVNI
SETGSVVLPRFFVDIIKKLPKGDVKLSTNEQFQTLITSGHSEFNLGSLDPDQYPLLPQVSRDDAIQLSV
KVLKNVIAQTNFAVSTSETRPVLTVGNWLIQENELICTATDSHRLAVRKLQLEDVSENKNV IIPGKALAE
LNKIMSDNEEDIDIFFASNQVLFKVGNVNFISSLLEGHPDTRLPENYEIKLSIDNGEFYHAIDRASL
LAREGGNNVIKLSLGDDVVELSSTSPEIGTVKEEVDANDVEGGLKISFNSKYMMMDALKAI DNDEVEVEF
FGTMKPFILPKGDDSVTLILPIRTY

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